

## AMENDMENTS

### *In the claims*

Please cancel claims 51-85 without prejudice or disclaimer.

Please add new claims 86-120.

86. (New) A substantially isolated polynucleotide comprising a sequence that encodes a polypeptide comprised of either or both of a H chain V region and L chain V region of an antigen binding polypeptide, wherein said antigen binding polypeptide competitively inhibits specific binding of an ScFv or antibody to a tumor cell epitope; wherein the ScFv or antibody is comprised of the amino acid sequences of the H chain V region and the L chain V region of the polypeptide in SEQ ID NO: 13, and wherein the antigen binding polypeptide specifically recognizes a cancer cell and does not recognize a normal non-cancerous cell.

87. (New) The polynucleotide of claim 86, wherein said antigen binding polypeptide specifically recognizes any one or more of at least glioma, melanoma, breast carcinoma, lung carcinoma, ovarian carcinoma, lymphoma, gastric carcinoma, colon carcinoma or prostate carcinoma cells, but does not recognize normal, non-cancerous cells of at least brain, skin, breast, lung, ovary, lymph node, large intestine and prostate tissues.

88. (New) The polynucleotide of claim 86, wherein said antigen binding polypeptide specifically recognizes a heptapeptide displayed by peptide phage display, said heptapeptide selected from the group consisting of:

Phe-His-Arg-Tyr-Ser-Leu-Pro (SEQ ID NO:20);

Phe-His-Arg-Tyr-Ser-Asp-Tyr (SEQ ID NO:21);

Phe-His-Arg-Tyr-Ser-Pro-Thr (SEQ ID NO:23);

Phe-His-Arg-Tyr-Thr-Pro-Gly (SEQ ID NO:24); and

Met-His-Arg-Tyr-Thr-Pro-Leu (SEQ ID NO:28).

89. (New) The polynucleotide of claim 86, wherein the antigen-binding polypeptide specifically recognizes an N-terminus pentapeptide consensus sequence Phe-His-Arg-Tyr-Ser/Thr (SEQ ID NO: 19) displayed as part of a heptapeptide by peptide phage display.

90. (New) The polynucleotide of claim 86, wherein the polynucleotide encodes at least 5 amino acids of either or both of the amino acid sequences of the H chain V region and the L chain V region of the polypeptide in SEQ ID NO: 13.

91. (New) The polynucleotide of claim 86, wherein the polynucleotide comprises at least 20 consecutive nucleotides of the sequence of either or both of the H chain V region and the L chain V region of the polynucleotide in SEQ ID NO: 13.

92. (New) The polynucleotide of claim 86, wherein the polynucleotide comprises a region of at least 20 consecutive nucleotides which is maintained in a stable duplex under stringent conditions with a complement of a second polynucleotide, wherein the second polynucleotide encodes a ScFv or antibody comprised of the amino acid sequences of the H chain V region and the L chain V region of the polypeptide in SEQ ID NO: 13, wherein stringent conditions comprise 0.1X SSC, 75% formamide, and incubation at 68°C.

93. (New) The polynucleotide of claim 92, wherein the polynucleotide comprises a region of at least 100 consecutive nucleotides which forms a stable duplex under stringent conditions with the complement of the second polynucleotide.

94. (New) The polynucleotide of claim 92, wherein the polynucleotide comprises a region of at least 200 consecutive nucleotides which forms a stable duplex under stringent conditions with the complement of the second polynucleotide.

95. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises a CDR region of the polypeptide in SEQ ID NO: 13.

96. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least five consecutive amino acid residues of the H chain CDR3 of the polypeptide in SEQ ID NO: 13.

97. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least six consecutive amino acid residues of the H chain CDR3 of the polypeptide in SEQ ID NO: 13.

98. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least seven consecutive amino acid residues of the H chain CDR3 of the polypeptide in SEQ ID NO: 13.

99. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least eight consecutive amino acid residues of the H chain CDR3 of the polypeptide in SEQ ID NO: 13.

100. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least five consecutive amino residues of the L chain CDR3 of the polypeptide in SEQ ID NO: 13.

101. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least six consecutive amino acid residues of the L chain CDR3 of the polypeptide in SEQ ID NO: 13.

102. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least seven consecutive amino acid residues of the L chain CDR3 of the polypeptide in SEQ ID NO: 13.

103. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least 25 amino acids of a variable region of the polypeptide in SEQ ID NO:13.

104. (New) The polynucleotide of claim 86, wherein the antigen binding polypeptide comprises at least 30 amino acids of a variable region of the polypeptide in SEQ ID NO:13.

105. (New) The polynucleotide of claims 86, wherein polynucleotide further encodes at least one chemically functional moiety.

106. (New) The polynucleotide of claim 105, wherein the at least one chemically functional moiety is selected from the group consisting of a signal peptide, an agent that enhances immunologic reactivity, an agent that facilitate coupling to a solid support, a carrier, a bioresponse modifier, a toxin, and a drug.

107. (New) The polynucleotide of claim 106, wherein the signal peptide is prokaryotic.

108. (New) The polynucleotide of claim 106, wherein the agent that enhances immunologic reactivity is a bacterial superantigen.

109. (New) The polynucleotide of claim 106, wherein the bioresponse modifier is a cytokine.

110. (New) The polynucleotide of claim 106, wherein the toxin is selected from the group consisting of ricin, pokeweed antiviral protein, Pseudomonas exotoxin A, diphtheria toxin, ricin A chain, restrictocin, and phospholipase enzymes.

111. (New) The polynucleotide of claim 86 or 87, wherein the antigen binding polypeptide is selected from the group consisting of whole native antibodies, bispecific antibodies, chimeric antibodies, Fab, F(ab')<sub>2</sub>, single chain V region fragments (scFv) and fusion polypeptides.

112. (New) The polynucleotide of claim 86 or 87, wherein said antigen binding polypeptide is an antigen binding polypeptide of a human antibody.

113. (New) The polynucleotide of claim 86 or 87, wherein the antigen binding polypeptide comprises human immunoglobulin sequences.

114. (New) The polynucleotide of claim 86 or 87, wherein said antigen binding polypeptide comprises human framework sequences.

115. (New) A cloning vector comprising a polynucleotide of claim 86.

116. (New) An expression vector comprising a polynucleotide of claim 86.

117. (New) A host cell comprising a polynucleotide of claim 86.

118. (New) A composition comprising a polynucleotide of claims 86.

119. (New) A process for making a polynucleotide of claim 86 comprising preparing the polynucleotide using one or method selected from: chemical synthesis, nucleic acid amplification, and recombinant cloning methods.

120. (New) A process for making an antigen binding polypeptide by expressing a polynucleotide of claim 86 in a host cell.